

obtaining the base sequence data at a front restriction enzyme site and the base sequence data at a back restriction enzyme site, as specified by corresponding to a restriction enzyme used for cleaving the vector and a restriction enzyme used for obtaining the object DNA fragment, from the database;

generating a first forward retrieval key using the obtained base sequence data of the front restriction enzyme site and a first backward retrieval key using the obtained base sequence data of the back restriction enzyme site;

retrieving base sequence data of the recombinant DNA obtained by a search using the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment; and

removing nucleic acid molecules of the vector at the specified junction.

24. (AS ONCE AMENDED) The method according to Claim 23,

wherein sequence data of the first forward retrieval key and of the first backward retrieval key are generated by base sequence data of the vector entered in a vector database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in the multiple cloning site,

wherein data of a forward base sequence from a cleaving point in the restriction enzyme site in the multiple cloning site of the vector are acquired from the database, and a second forward retrieval key is generated using the acquired forward base sequence data of the cleaving point of the restriction enzyme site of the vector,

performing first homology retrieval on condition that a first similarity value between retrieval base sequence data of the recombinant DNA and the first forward and first

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backward retrieval keys is equal to or larger than a predetermined value,

obtaining a candidate for a base sequence at the junction between the vector and the object DNA fragment according to a result of the first homology retrieval, and

performing a second homology retrieval on condition that a second similarity value between base sequence data of a plurality of first candidates for the junction, and base sequence data of the second forward retrieval key, is equal to or larger than a predetermined value.

25. (AS ONCE AMENDED) The method according to Claim 23,

wherein the sequence data of the first forward retrieval key and of the first backward retrieval key are generated by base sequence data of the vector entered in a vector database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in the multiple cloning site,

wherein forward base sequence data of a forward cleaving point of the restriction enzyme site of the vector, and backward base sequence data of a backward cleaving

point of the vector are acquired from the database, and a second forward retrieval key and a second backward retrieval key are generated using the base sequence data of the acquired forward and backward base sequence data of the cleaving points, respectively,

performing a first homology retrieval on condition that a first similarity value between retrieval base sequence data of the recombinant DNA and the first forward and first backward retrieval keys is equal to or larger than a predetermined value,

obtaining a candidate for a base sequence at the junction between the vector and the object DNA fragment according to a result of the first homology retrieval, and

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performing a second homology retrieval on condition that a second similarity value between base sequence data of a plurality of first candidates for the junction, and base sequence data of the second forward retrieval key, is equal to or larger than a predetermined value.

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26. (AS ONCE AMENDED) The method according to Claim 25, wherein the sequence data of the first forward and first backward retrieval keys are generated by base sequence data of the vector entered in a vector database, data of a multiple cloning site in the vector, and data of a restriction enzyme site in the multiple cloning site, and wherein the second homology retrieval is performed using both the second forward and second backward retrieval keys.

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28. (AS ONCE AMENDED) The method according to Claim 23, wherein backward base sequence data from a cleaving point in a multiple cloning site of the vector corresponding to the restriction enzyme are acquired from the database, and a second backward retrieval key is generated using the acquired backward base sequence data of the cleaving point, and performing a first homology retrieval on condition that a first similarity value between retrieval base sequence data of the recombinant DNA and the first forward and first backward retrieval keys is equal to or larger than a predetermined value; obtaining a candidate for a base sequence at a junction between the vector and the object DNA fragment according to a result of the first homology retrieval; and performing a second homology retrieval on condition that a second

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similarity value between base sequence data of a first candidate for the junction, screened by using the first retrieval keys, and base sequence data of the second backward retrieval key is equal to or larger than a predetermined value.

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29. (AS ONCE AMENDED) The method according to Claim 28,
wherein said nucleic acid molecules of said vector are removed from the recombinant DNA sequence data, when the area specified by the second homology retrieval is one.

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30. (AS ONCE AMENDED) The method according to Claim 25, further comprising:
obtaining, as a forward vector unit candidate for the vector base sequence, a forward base sequence selected by the second homology retrieval, and a base sequence before said forward base sequence; and
obtaining, as a backward vector unit candidate for the vector base sequence, a backward base sequence selected by the second homology retrieval, and a base sequence after said backward base sequence.

SUB C29

31. (AS ONCE AMENDED) The method according to Claim 29,
wherein said forward vector unit candidate and said backward vector unit candidate are removed from the recombinant DNA sequence data, when there is only one candidate respectively for the specified forward and backward vector units, and the specified forward and backward vector units do not overlap each other.

32. (AS ONCE AMENDED) A device for removing nucleic acid molecules of a vector from a recombinant DNA base sequence, obtained as a result of performing a cloning process by integrating an object DNA fragment into a vector, comprising:

a database storing data identifying each of restriction enzymes, and data of base sequences at a plurality of restriction enzyme sites of a plurality of vectors correspondingly;

an obtaining unit obtaining base sequence data at a front restriction enzyme site and base sequence data at a back restriction enzyme site, as specified corresponding to a restriction enzyme used for cleaving the vector and a restriction enzyme used for obtaining the object DNA fragment, from the database;

a generation unit generating a first forward retrieval key using the obtained base sequence data of the front restriction enzyme site, and a first backward retrieval key using the obtained base sequence data of the back restriction enzyme site; and

a retrieving unit retrieving base sequence data of the recombinant DNA obtained using the first forward and first backward retrieval keys, and specifying a junction between the vector and the object DNA fragment.

33. (AS ONCE AMENDED) The device according to Claim 32, further comprising:

display means,

wherein said vector is included in a vector list displayed on said display means, and

wherein at least one of said specified restriction enzymes is included in a restriction enzyme list displayed on said display means.

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34. (AS ONCE AMENDED) The device according to Claim 32, further comprising:

program storage means for storing at least one of:

a program for generating the retrieval keys by controlling said generation unit;

a program for specifying the vector base sequence by controlling said retrieving unit; and

a program for removing the vector base sequence.

35. (AS ONCE AMENDED) The device according to Claim 32,

wherein said retrieving unit specifies using the first retrieval key as a junction between the vector base sequence data and the object DNA fragment sequence data.

36. (AS ONCE AMENDED) The device according to Claim 35,

wherein said retrieving unit specifies, as the junction, a portion in the DNA base sequence data in which a number of bases matching a base sequence of the first retrieval key is equal to or larger than a predetermined value.

37. (AS ONCE AMENDED) The device according to Claim 32,

wherein said retrieving unit specifies using, as the first retrieval key, a first junction and a second junction between the vector base sequence and the object DNA fragment.

38. (AS ONCE AMENDED) The device according to Claim 32,

wherein each of said first forward and first backward retrieval keys

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includes sequence data including an end portion of the object DNA fragment and sequence data including an end portion of the vector base sequence, and specifies a candidate for the junction between the vector base sequence and the object DNA fragment.

39. (AS ONCE AMENDED) The device according to Claim 38,
wherein a second retrieval key, including sequence data longer than that
of said first forward and first backward retrieval keys, is generated, and the junction is specified
using the second retrieval key.

40. (AS ONCE AMENDED) The device according to Claim 39,
wherein said object DNA fragment is specified by removing the junction
and sequence data distal to the junction and the object DNA fragment from the DNA base
sequence.

41. (AS ONCE AMENDED) A computer-readable storage medium on which is
recorded a program enabling a computer to execute an operation process of a base sequence
of a recombinant DNA obtained by integrating an object DNA into a vector, said process
comprising the steps of:

storing data identifying each of restriction enzymes and data of base
sequences at a plurality of restriction enzyme sites of a plurality of vectors correspondingly, in a
database;

obtaining base sequence data at a front restriction enzyme site and base
sequence data at a back restriction enzyme site, as specified corresponding to a restriction